SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: OKAMURA, Haruki TANIMOTO, Tadao TORIGOE, Kakuji KUNIKATA, Toshio TANIGUCHI, Mutsuko KOHNO, Keizo KURIMOTO, Masashi
- (ii) TITLE OF INVENTION: IFN-BETA PRODUCTION INDUCING PROTEIN AND MONOCLONAL ANTIBODY OF THE SAME
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BROWDY AND NEIMARK
 - (B) STREET: 419 Seventh Street, N.W., Suite 300
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20004
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk

 - (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/502,535
 (B) FILING DATE: 14-JUL-1995
 (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 184162/1994
 - (B) FILING DATE: 14-JUL-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 45057/1995
 (B) FILING DATE: 10-FEB-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BROWDY, Roger L.

 - (B) REGISTRATION NUMBER: 25,618
 (C) REFERENCE/DOCKET NUMBER: OKAMURA=2
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-628-5197
 - (B) TELEFAX: 202-737-3528
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS -
 - (B) LOCATION: 1..471

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	(xi)	SEQ	UENC	E DE	SCRI	PTIC	N: S	EQ I	D NO	:1:								
AAC Asn 1	TTT Phe	GGC Gly	CGA Arg	CTT Leu 5	CAC His	TGT Cys	ACA Thr	ACC Thr	GCA Ala 10	GTA Val	ATA Ile	CGG Arg	AAT Asn	ATA Ile 15	AAT Asn			48
GAC Asp	CAA Gln	GTT Val	CTC Leu 20	TTC Phe	GTT Val	GAC Asp	AAA Lys	AGA Arg 25	CAG Gln	CCT Pro	GTG Val	TTC Phe	GAG Glu 30	GAT Asp	ATG Met			96
ACT Thr	GAT Asp	ATT Ile 35	GAT Asp	CAA Gln	AGT Ser	GCC Ala	AGT Ser 40	GAA Glu	CCC Pro	CAG Gln	ACC Thr	AGA Arg 45	CTG Leu	ATA Ile	ATA Ile		:	144
TAC Tyr	ATG Met 50	TAC Tyr	AAA Lys	GAC Asp	AGT Ser	GAA Glu 55	GTA Val	AGA Arg	GGA Gly	CTG Leu	GCT Ala 60	GTG Val	ACC Thr	CTC Leu	TCT Ser			192
GTG Val 65	Lys	GAT Asp	AGT Ser	AAA Lys	AYG Xaa .70	TCT Ser	ACC Thr	CTC Leu	TCC	TGT Cys 75	AAG Lys	AAC Asn	AAG Lys	ATC Ile	ATT Ile 80			240
TCC Ser	TTT Phe	GAG Glu	GAA Glu	ATG Met 85	GAT Asp	CCA Pro	CCT Pro	GAA Glu	AAT Asn 90	ATT Ile	GAT Asp	GAT Asp	ATA	CAA Gln 95	AGT Ser			288
Asp	Leu	ATA	Phe 100	Phe	Gln	Lys	Arg	Val 105	Pro	Gly	His	Asn	110	Met	GIU			336
TTT Phe	GAA Glu	TCT Ser 115	Ser	CTG Leu	TAT	GAA Glu	GGA Gly 120	His	TTT: Phe	CTT Leu	GCT Ala	TGC Cys 125	GIT	A AAC 1 Lys	GAA Glu	*	•	384
GAT Asi	GAT Asp 130	GCT Ala	TTC Phe	AAA Lys	CTC Leu	ATT 11e 135	. Lev	AAA Lys	AAA E Lys	A AAG S Lys	GAT ASP 140	Glu	AA A	r GG(n Gly	G GAT Y Asp			432
AA) Lys 14	s Sei	r GTA	A ATG L Met	TTC Phe	ACT Thr	: Lev	ACT Thi	OAA 7	TT/	A CAT 1 His 155	s Glr	A AGT n Ser						47.
(2) IN	FORM			·								i en					
		(i)	SEQU		E CHA					ds			•					

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
- Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg Asn Ile Asn 10 15
- Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe Glu Asp Met 20 25 30
- Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg Leu Ile Ile 40 45
- Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val Thr Leu Ser

Val 65	Lys	Asp	Ser	Lys	Xaa 70	Ser	Thr	Leu	Ser	Cys 75	Lys	Asn	Lys	Ile	Ile 80	1	*	
Ser	Phe	Glu	Glu	Met 85	Asp	Pro	Pro	Glu	Asn 90	Ile	Asp	Asp	Ile	Gln 95	Ser			
Asp	Leu	Ile	Phe 100	Phe	Gln	Lys	Arg	Val 105	Pro	Gly	His	Asn	Lys 110	Met	Glu	••••		•
Phe	Glu	Ser 115	Ser	Leu	Tyr	Glu	Gly 120		Phe	Leu	Ala	_Cys 125	Gln	Lys	Glu		· .	
Asp	Asp 130	Ala	Phe	Lys	Leu	Ile 135	Leu	Lys	Lys	Lys	Asp 140	Glu	Asn	Gly	Asp	•		
Lys 145	Ser	Val	Met	Phe	Thr 150	Leu	Thr	Asn	Leu	His 155	Gln	Ser	•					
(2)	INF	ORMA	TION	FOR	SEQ	ID	NO:3	:	٠.			•	٠.		•			
	(i	(QUEN A) L B) T C) S D) T	ENGT YPE: TRAN	H: 2 nuc DEDN	0 ba leic ESS:	se p aci sin	airs .d	•			•						
	(ii) MC	LECU A) D	LE I	YPE: IPTI	oth ON:	er r /des	ucle sc =	eic a "Oli	icid .gonu	clec	tide	; n ·	-		•		
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· 5.00	-					LIPII	LON.	SEQ	10 1	.0.5								2 0
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(2)) SI	EQUEN (A) I (B) 3 (C) 2 (D) 3	ICE (LENGT LYPE STRAI	HARA H: 2 nuc	ACTEI 20 ba cleio NESS	RIST ase p c ac: : si	ICS: pair: id	s ·,				:					
e species .	(i:	i) M	OLECI	DESC	TYPE RIPT	otl	her /de	nucl sc =	eic "Ol	acid igon	ucle	otid	e"			 . .	المستعرب	
	(x.	i) s	EQUE	NCE :	DESC	RIPT	ION:	SEQ	ID	NO : 4							• .	
TT	YGAR	GAYA	TGA	CNGA	YAT .					.74								2
(2) IN	FORM	ATIO	й FO	R SE	Q ID	NO:	5: -					, in give			- - ; .	* <u>*</u> .	
	(i) S	(B). (C)	NCE LENG TYPE STRA TOPO	TH: : nu NDED	17 b clei NESS	ase c ac : si	pair id ngle	s			٠,						
,	(i	i) M	OLEC (A)	ULE DESC	TYPE RIPT	: ot	her /de	nucl esc =	leic = "Ol	acid igor	l nucle	otic	le"	10.4	,	•; ••.		
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TTYGARGARA TGGAYCC

(2) INFORMATION FOR SEQ ID NO:6:

	(A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear		-		
(ii) M	OLECULE TYPE: cDNA	•		•	
2.5				,	
(xi) S	SEQUENCE DESCRIPTION: SEQ ID	NO:6:			
CGAGGGATC	AACTTTGGCC GACTTC	_	,,,		- 26
(2) INFORM	MATION FOR SEQ ID NO:7:				
(i) s	SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS:/single (D) TOPOLOGY: linear				
(ii) 1	MOLECULE TYPE: cDNA				
(xi)	SEQUENCE DESCRIPTION: SEQ ID	NO:7:			•
CGAGGAATT	C CTAACTTTGA TGTAAG			. ,	20
(2) INFOR	MATION FOR SEQ ID NO:8:		. •		
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear				
(ii)	MOLECULE TYPE: cDNA	*.	in the same of the	•	
(xi)	SEQUENCE DESCRIPTION: SEQ ID	NO:8:			•
GAGGAATTO	CT GGAGGAAGGT ACCATGAACT TTGG	CCGACT TC			- 4
(2) INFO	RMATION FOR SEQ ID NO:9:				
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear				-
(ii)	MOLECULE TYPE: cDNA	•	•		
		•			

(i) SEQUENCE CHARACTERISTICS:

26

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGAAAGCTT CTAACTTTGA TGTAAG